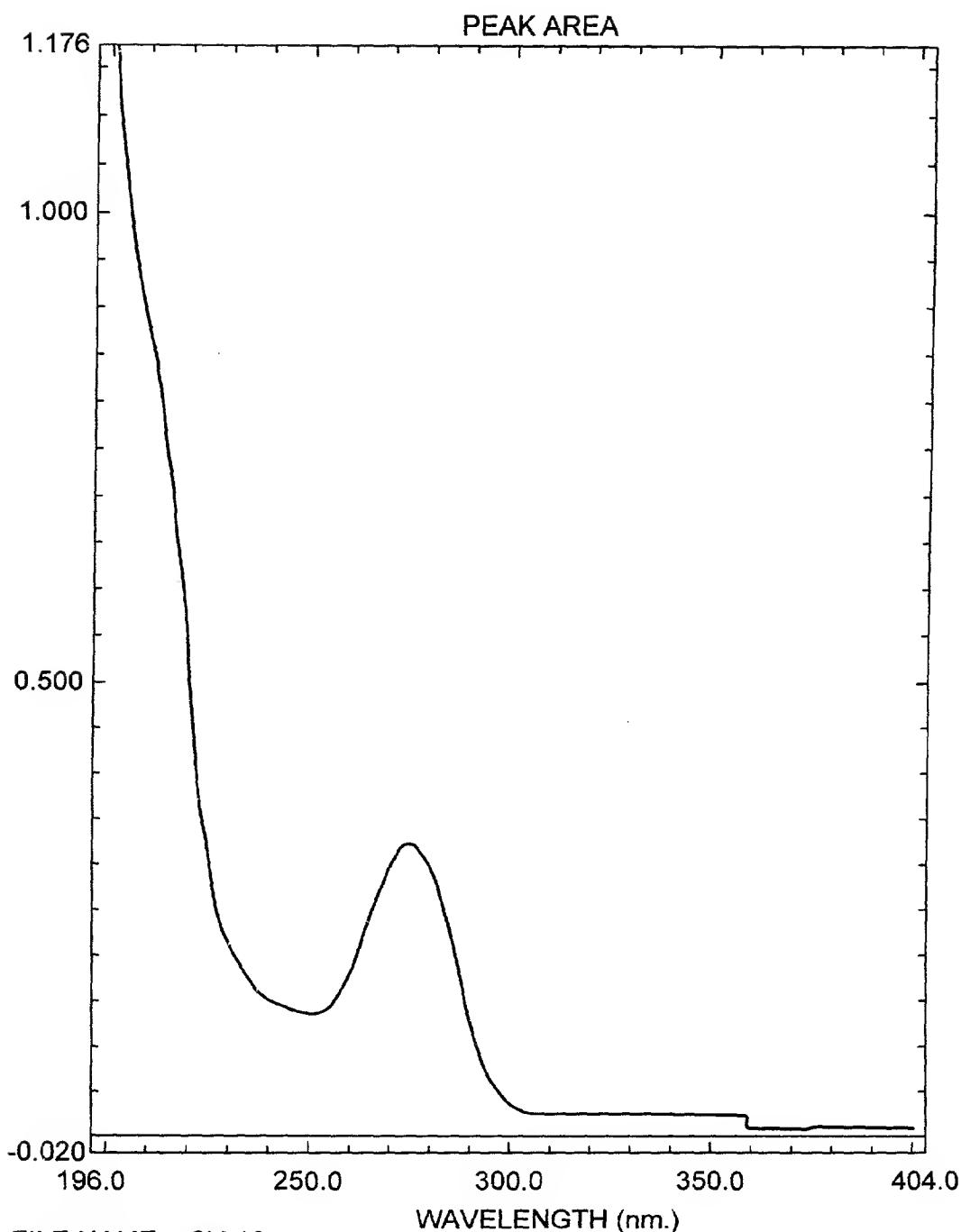


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CREATED: 14:29 01-01-22
DATA: ORIGINAL
MEASURING MODE: ABS.
SCAN SPEED: FAST
SLIT WIDTH: 1.0
SAMPLING INTERVAL: 0.2
RESULT - (AREA-FACTOR) DIVISOR FACTOR = 9.999
REGIUM START END DIVISOR AREA RESULT

FIG. 1

*****CAMAGILC Evaluation Software*****

ARBRO PHARMACEUTICALS LTD 6/14 KIRTI NAGAR INDUSTRIAL AREA NEW DELHI
PHONE: 5467228.515-0437. FAX: 91-11-5463784, E-mail: arbo@vsn1.com

TLC/HPTLC-Integration (CATS3.18 S/N:0207A004 / SCANNER II V3.14 S/N:990602)

ESTIMATION OF L-LYSINE BY HPTLC

Calibr. Table Calibration Table created: ARBRO PHARMA LTD

File name: AMINO 3/JUN/ 0 14:49:46

Scan User name while measuring : ARBRO PHARMA LTD

File name: AMINO 3/JUN/ 0 14:54:52

INTEGRATION User while integrating: ARBRO PHARMA LTD

File name: AMINO 3/JUN/ 0 15:19:26

Track 1. Analysis a:

Peak #	start mm	h mm	max h	a [%]	end mm		a [%]	area
					mm	h		
1	61.1	0.4	72.6	64.1	100.00	78.2	0.1	3186.2 100.00
			Total height =	64.1			Total area =	3186.2

Track 2. Standard level 1:

Peak #	start mm	h mm	max h	a [%]	end mm		a [%]	area
					mm	h		
1	62.9	2.8	71.0	63.5	100.00	78.8	0.0	3133.9 100.00
			Total height =	63.5			Total area =	3133.9

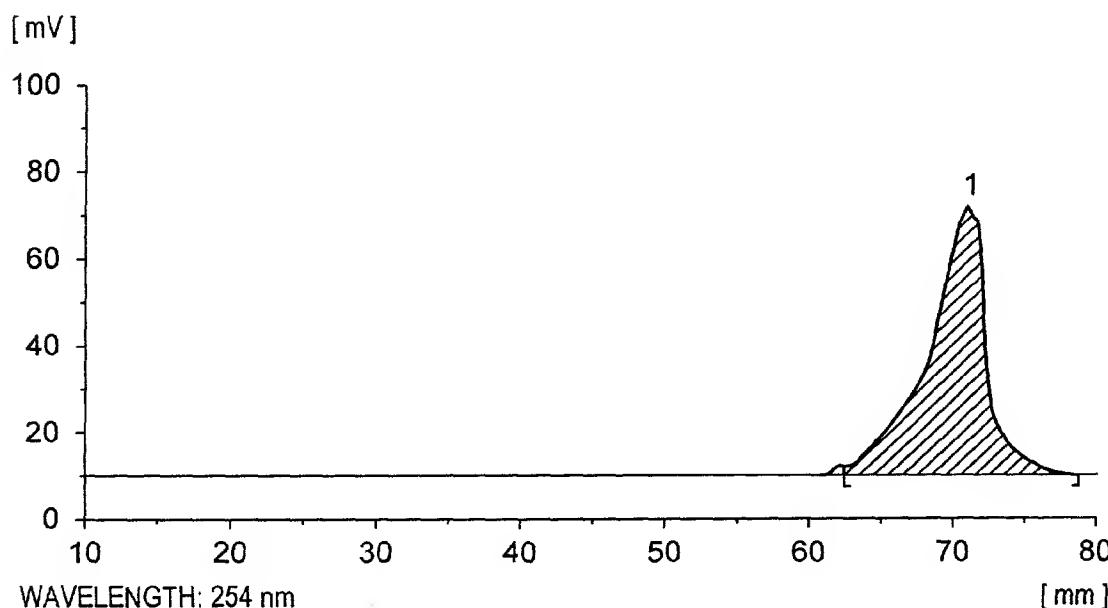
F I G. 2A

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U 013488-3

CALIBRATION : H : AMINO ARBRO PHARMA LTD
METHOD SCAN **INTEGRATION** CALIBRATION DATA END

3/JUN/2000 15:05
HELP

STANDARD LEVEL 1



TRACK: 2, NOISE LEVEL: 0.108mV, RAW DATA FILE: AMINO
CATS3.18 S/N: 0207A004 CAMAG SOFTWARE (c) 1996 SCANNER II: 990602

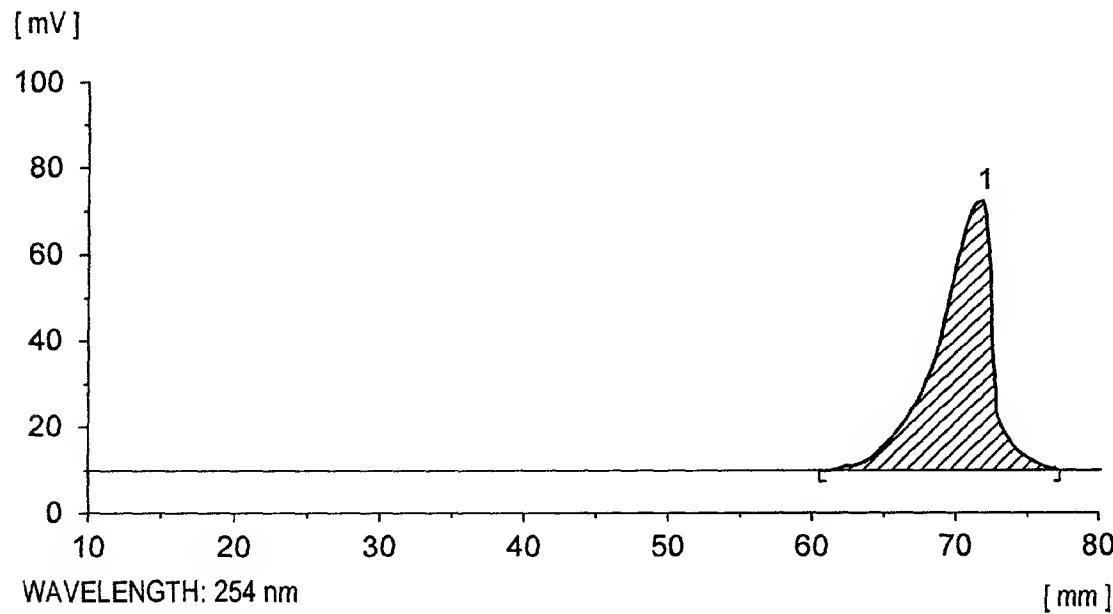
TRACK 2. STANDARD LEVEL 1

PEAK #	START		MAX			END		AREA	
	mm	h	mm	h	[%]	mm	h	a	[%]
1	62.9	2.8	71.0	63.5	100.00	78.8	0.0	3133.9	100.00
TOTAL HEIGHT = 63.5					TOTAL AREA = 3133.9				

F I G. 2b

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U 013488-3

CALIBRATION : H : AMINO ARBRO PHARMA LTD 3/JUN/2000 15:10
METHOD SCAN INTEGRATION CALIBRATION DATA END HELP
STANDARD LEVEL 1



TRACK: 1, NOISE LEVEL: 0.108mV, RAW DATA FILE: AMINO
CATS3.18 S/N: 0207A004 CAMAG SOFTWARE (c) 1996 SCANNER II: 990602

TRACK 1. ANALYSIS a:

PEAK	START		MAX			END		AREA		
	#	mm	h	mm	h	[%]	mm	h	a	[%]
1	1	61.1	0.4	72.6	64.1	100.00	78.2	01	3186.2	100.00
TOTAL HEIGHT = 64.1					TOTAL AREA = 3186.2					

F I G. 2c

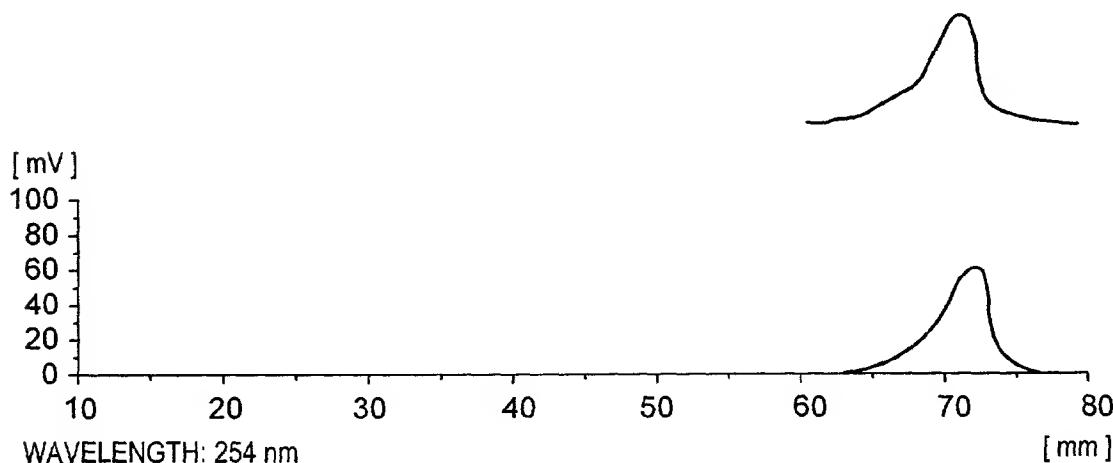
09/881,569
U 013488-3

CALIBRATION : H : AMINO ARBRO PHARMA LTD
METHOD SCAN **INTEGRATION** CALIBRATION DATA END 3/JUN/2000 15:20
HELP

STANDARD LEVEL 1



CALIBRATION : H : AMINO ARBRO PHARMA LTD
METHOD SCAN **INTEGRATION** CALIBRATION DATA END 3/JUN/2000 15:32
HELP



WAVELENGTH: 254 nm
FILE NAME: AMINO TRACK 1 TO 2
CATS3.18 S/N: 0207A004 CAMAG SOFTWARE (c) 1996 SCANNER II: 990602

FIG. 2d

SUBMITTER: PUSHPA KHANNA

SAMPLE NAME: GOURDIN

DATE:

SEQUENCE: HIS
CYCLE #: ASP LEU TYR SER GLN GLN VAL GLY — SER GLN — GLN ARG
1 2 3 4 5 6 7 8 9
VAL SER GLU GLU THR THR GLY — THR LEU

SEQUENCE: ARG
CYCLE #: LYS TYR HIS HIS ARG ASP ARG ARG
10 11 12 13 14 15 16 17 18
ARG — LEU — LYS — TYR — ASN — MET ASN THR HIS
LEU ALA GLU ASN ASP ILE — LEU — ASP — ALA

SEQUENCE: PRO
CYCLE #: SER GLU SER GLU THR ARG HIS
19 20 21 22 23 24 25 26 27
LEU ARG PRO ILE LEU PHE SER ALA ARG
LYS — GLU — ALA — ASP — ILE — TYR — ASN — HIS — GLY

SEQUENCE: PRO
CYCLE #: GLY VAL PRO
28 29 30 31 32 33 34 35
ALA — GLY — ARG — ILE — SER — THR — VAL — ASN
LEU ASN ILE ALA

YIELD(pmol): ILE(2) 98.11 YIELD(pmol): GLU(3) 56.13

CARRYOVER: ILE(6) 22.6% REP YIELD: ILE(2.23) 92.3%

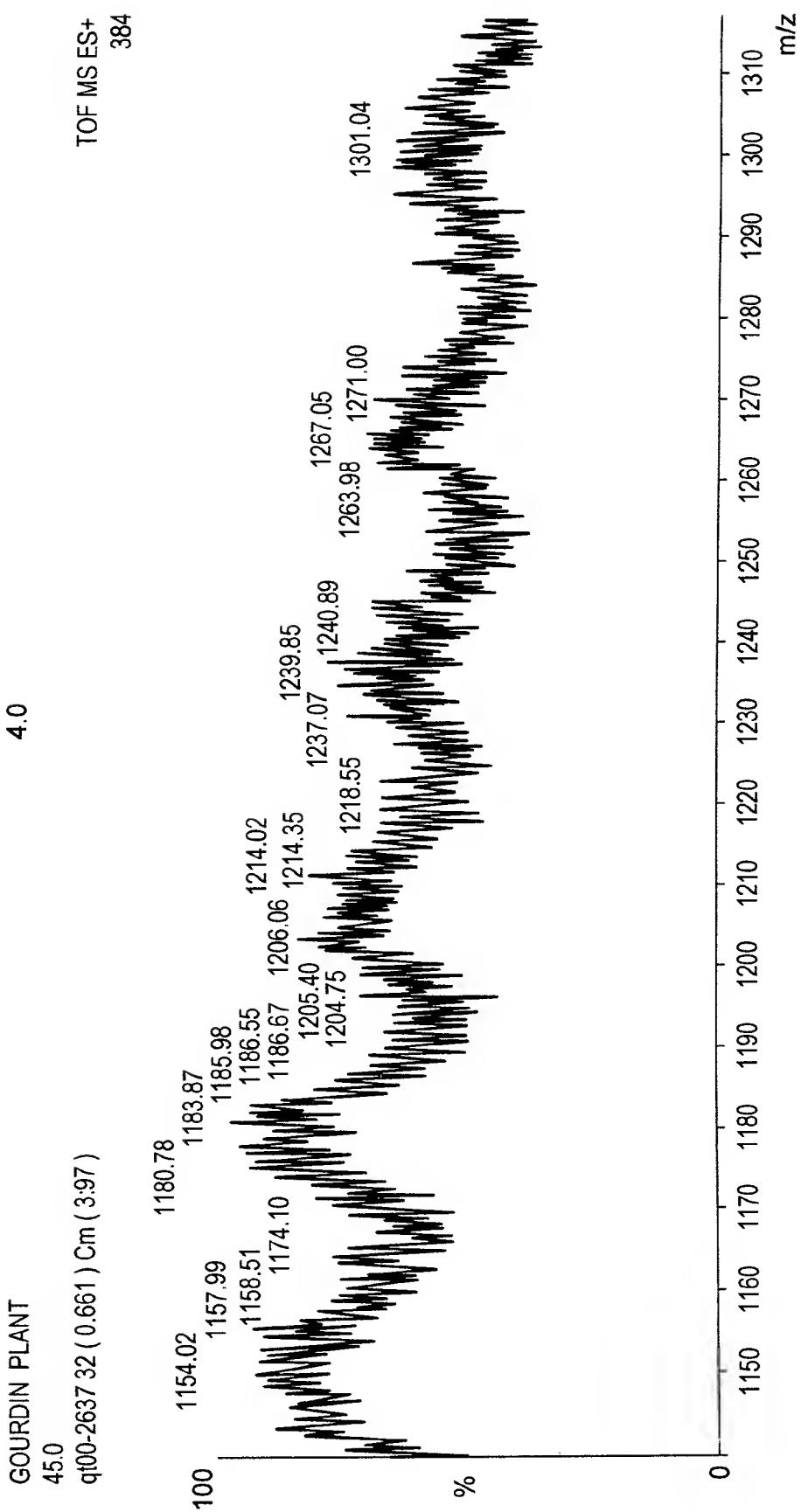
SEQSTD YIELD: NL(6) 2.30 SEQSTD CARRYOVER: NL(6) 23.0%

SEQSTD REP YIELD: NL(6.11) 97.0%

COMMENTS: Mixtures with interchangeable amino acid at positions 12,13,15-19, 25-27 and 31-34.
Appears to be a mixture of sequences.

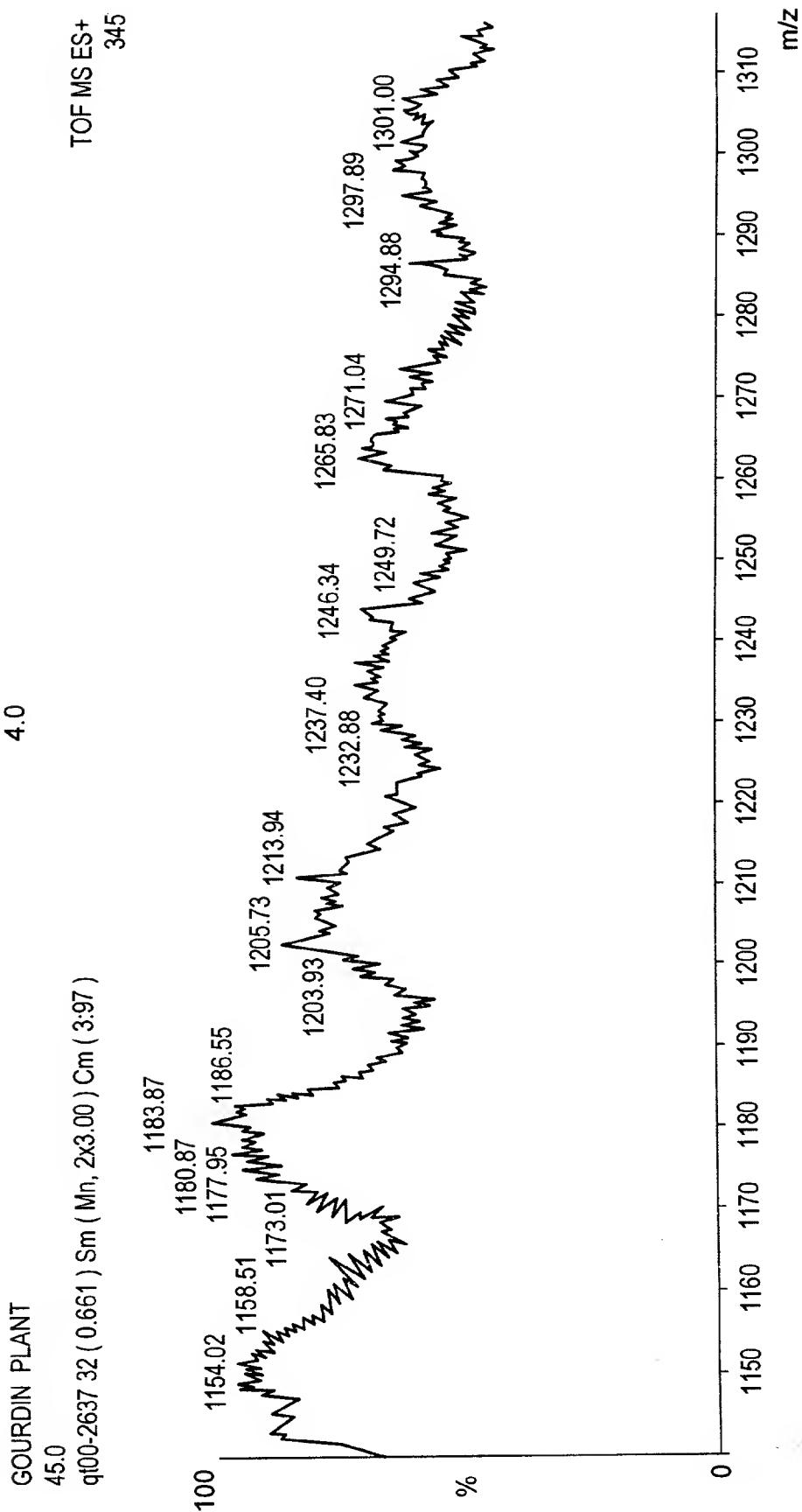
F I G. 3a

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U 013488-3



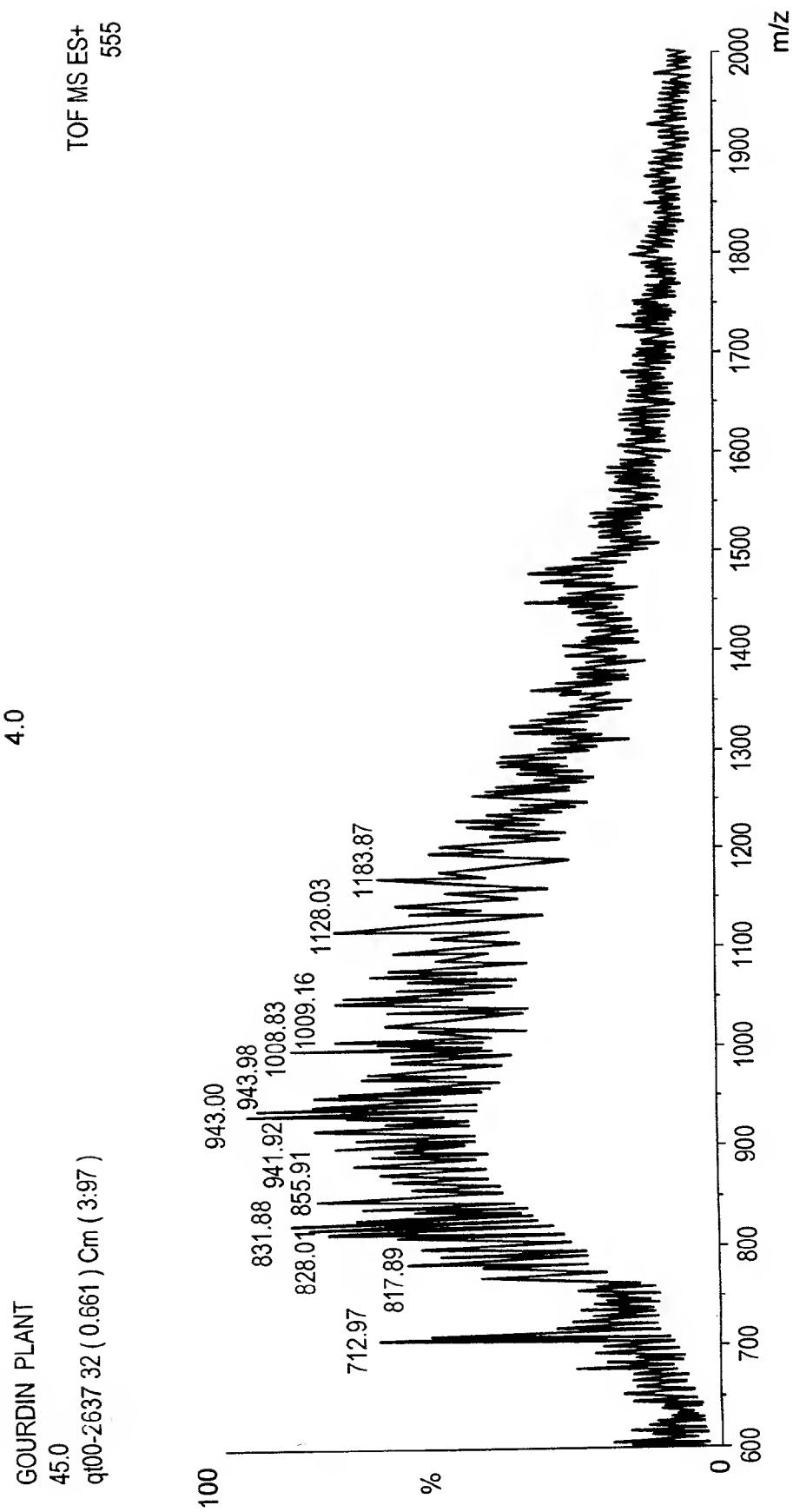
F | G. 4a1

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F | G. 4a2

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U 013488-3



F I G. 4b1

09/881,569
U 013488-3

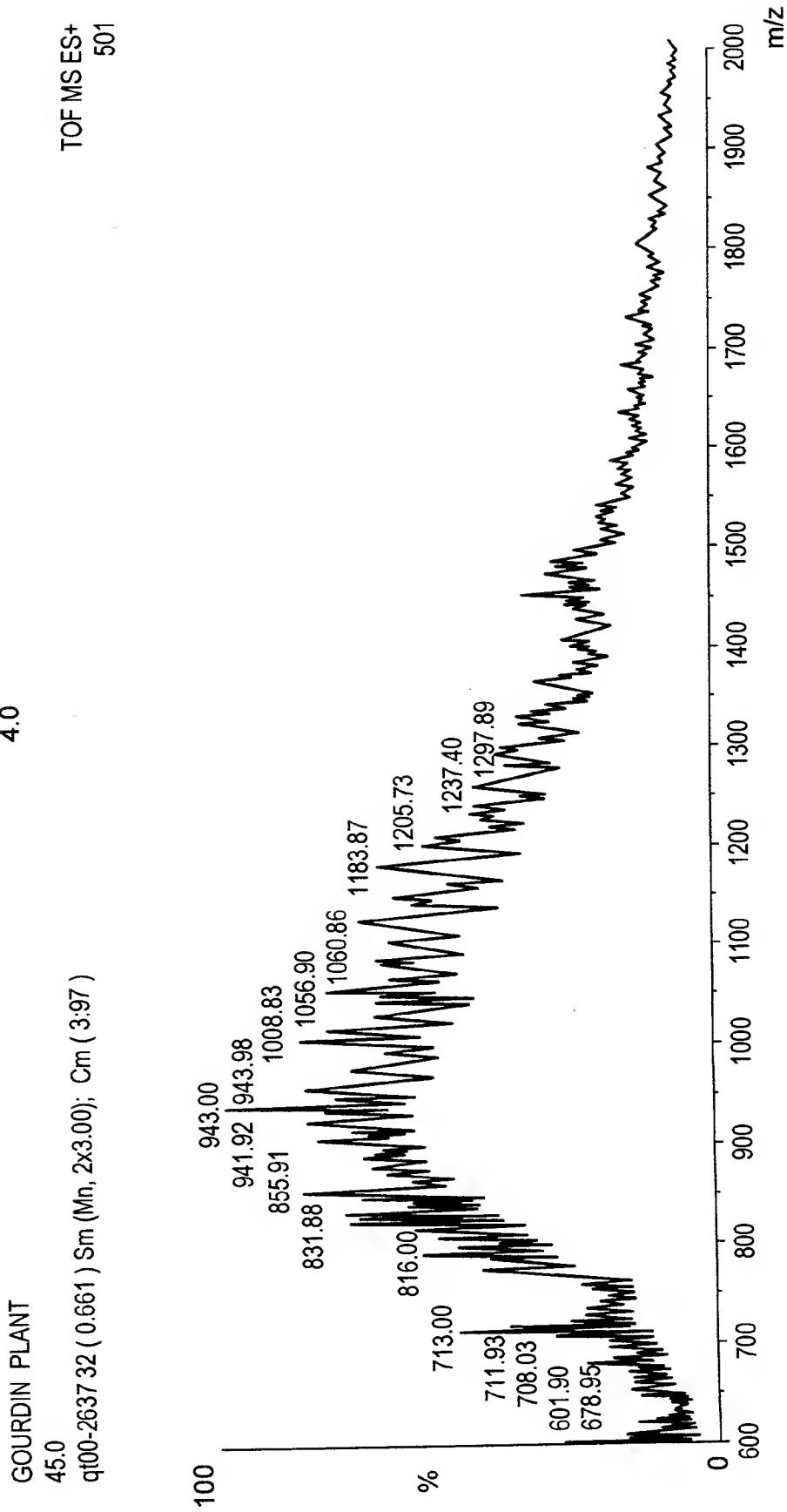
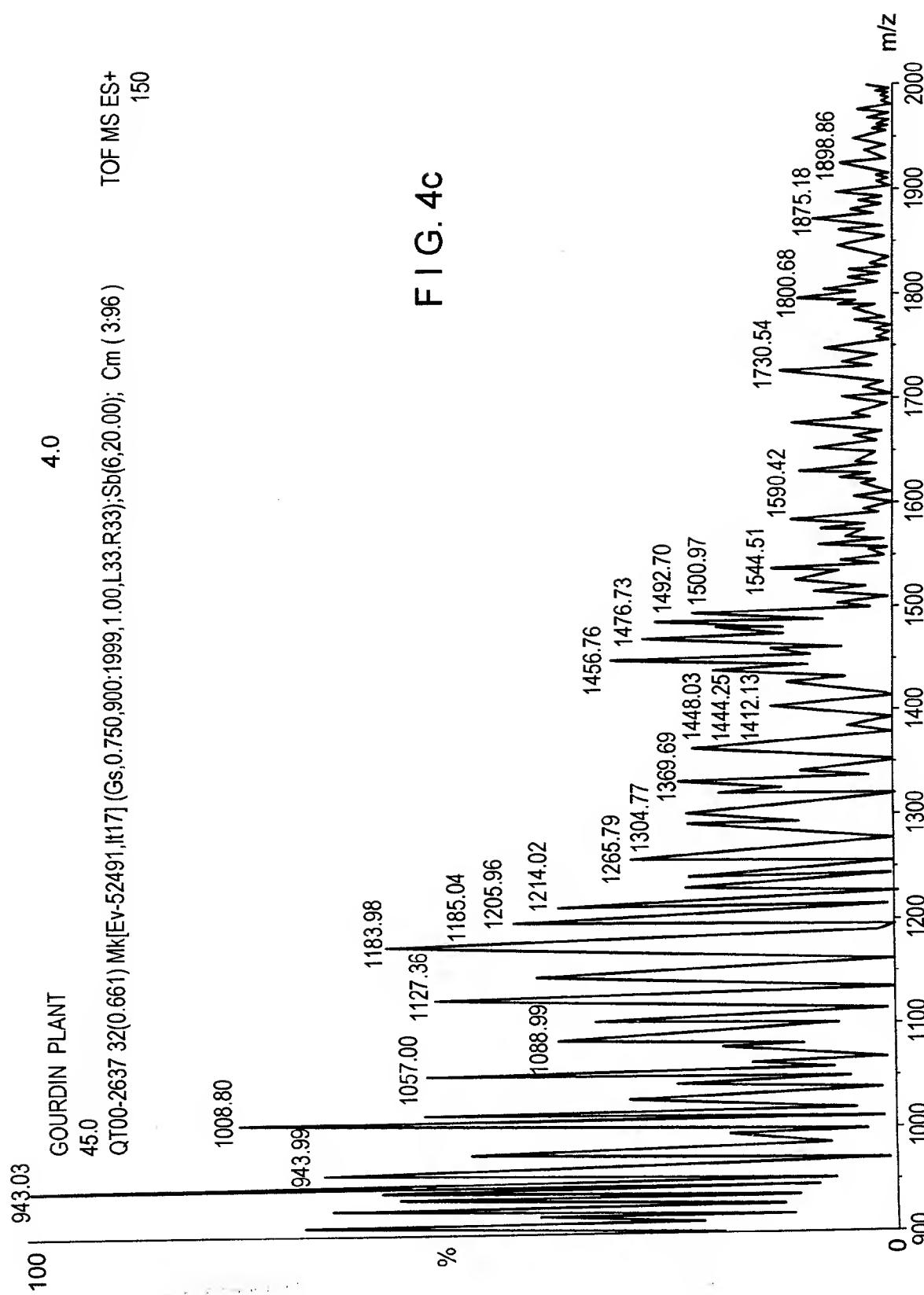
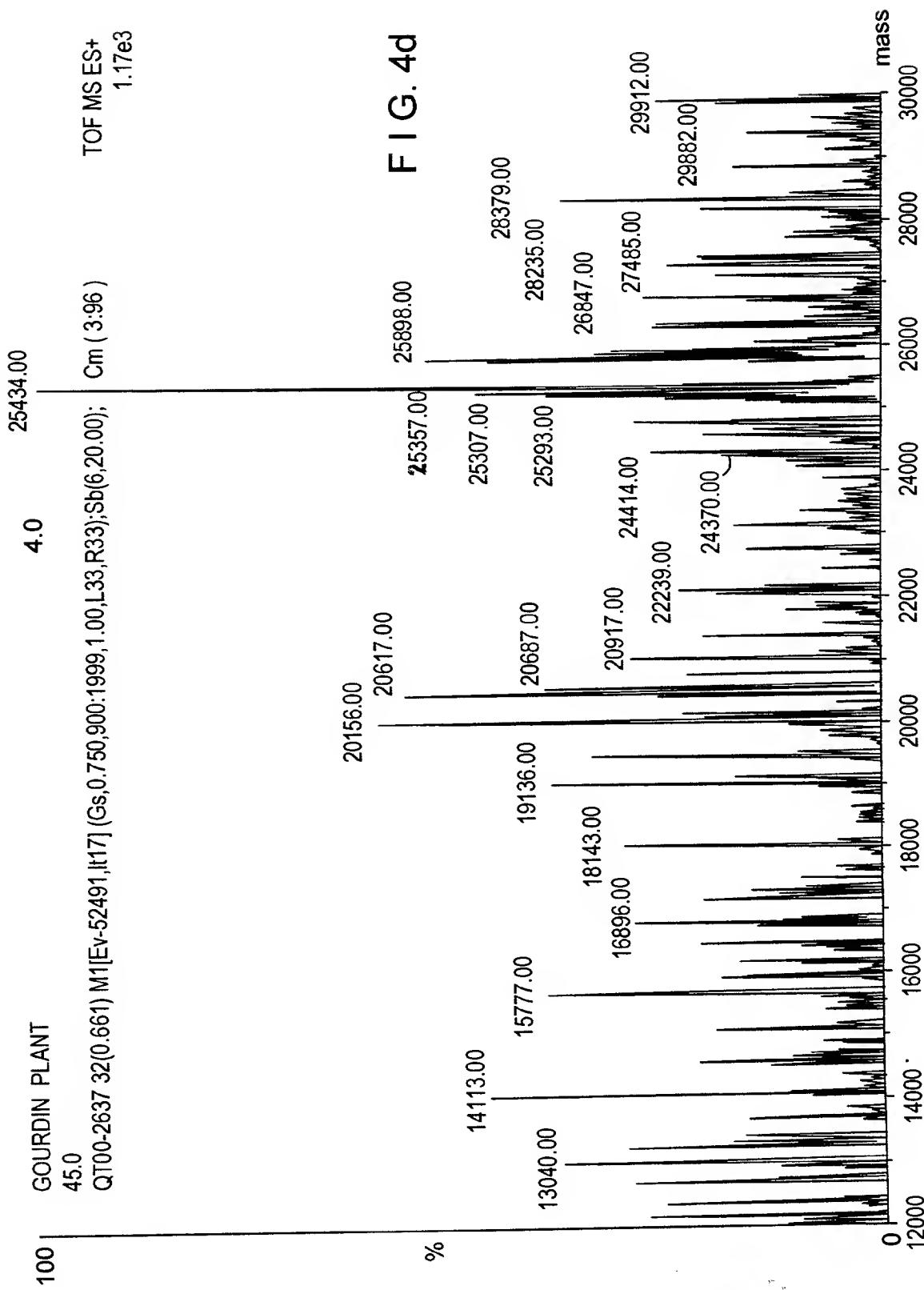


FIG. 4b2

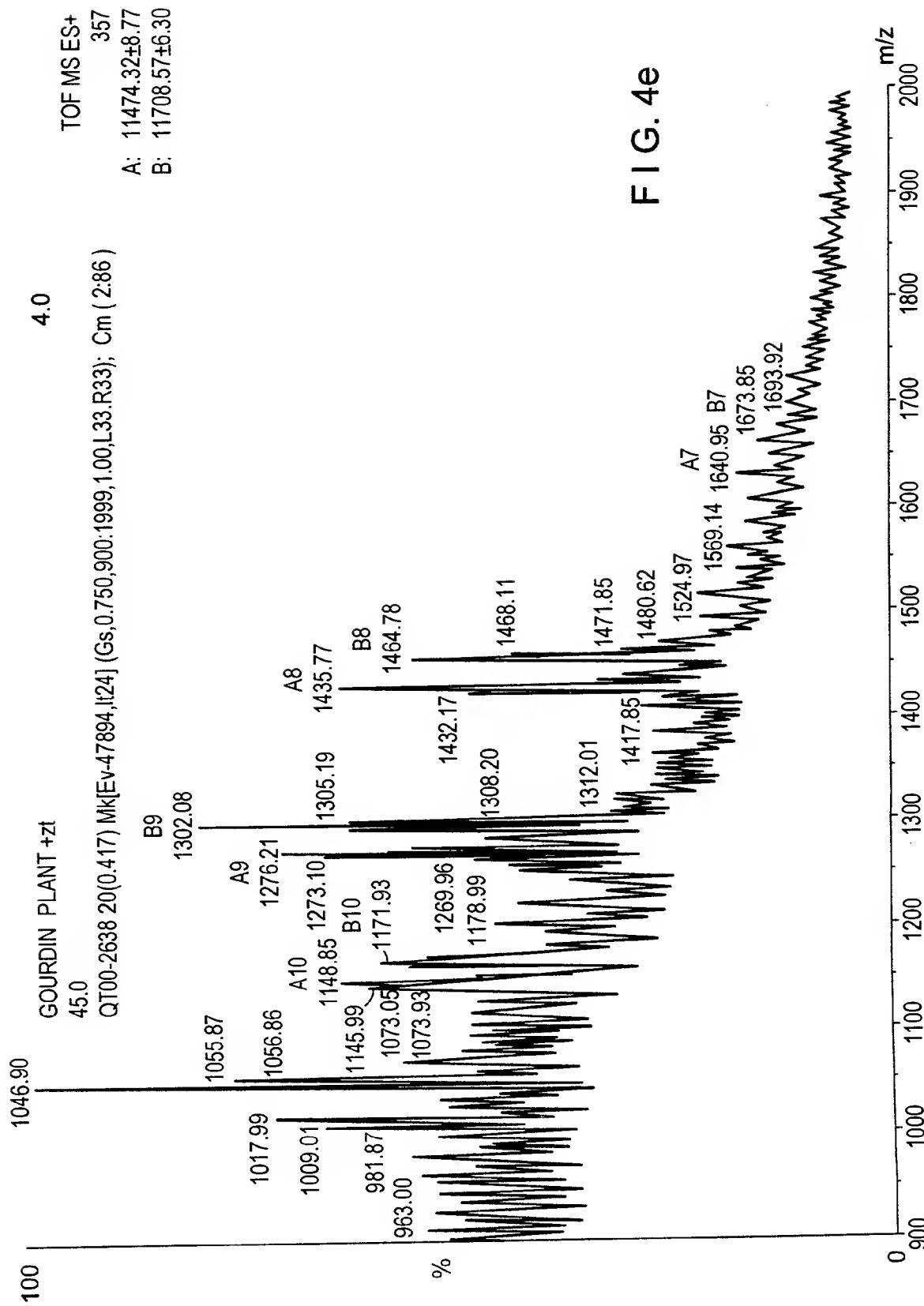
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U 013488-3



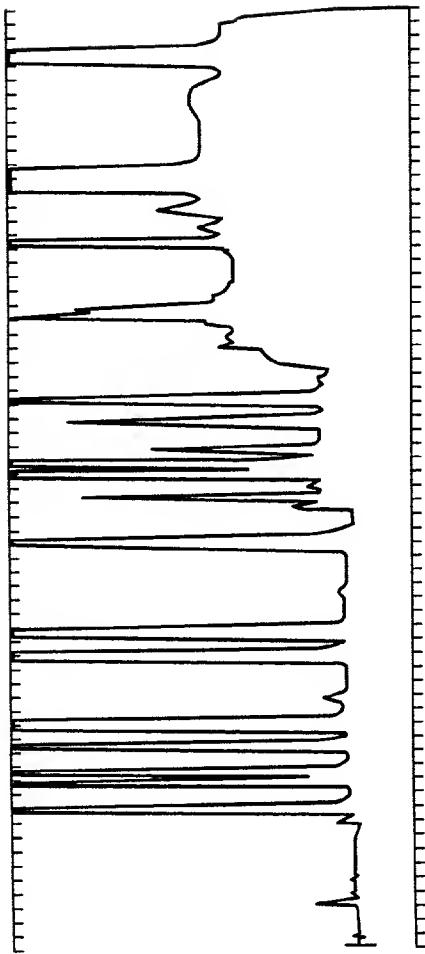
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U 013488-3



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U 013488-3



INTERFACE 01 0-68 Min SCALE: 15 Mv Ch. A, 15 Mv Ch. B
AMINO ACID ANALYSIS PROCESSED: 11-22-2000 14:26:30, SEGMENT 17, CYCLE 936
RAW DATA SAVED IN FILE K : AAA936.PTS SECOND CHANNEL STORED IN K : BAA936.PTS

EXTERNAL STANDARD TABLE

***** 11-22-2000 14 : 26 : 30 Version 4.1 *****
Data File: K:AAA936
Sample Name: amino acid analysis
Date: 11-22-2000 14 : 26 : 30 Method: F:REBECKA
Interface: 0 Cycle #: 936 Operator jmc Channel #: 0 Vial #: N.A.
Starting Peak Width: 21 Threshold: .5 Area Threshold: 500

Starting Delay: 0.00 Ending retention time: 68.00
Area reject: 5000 One sample per: 2.002 sec.
Amount injected: 1.00 Dilution factor: 1.00
Sample weight: 1.000000

F I G. 5a1

SEE FIG. 5a2

SEE FIG. 5a1

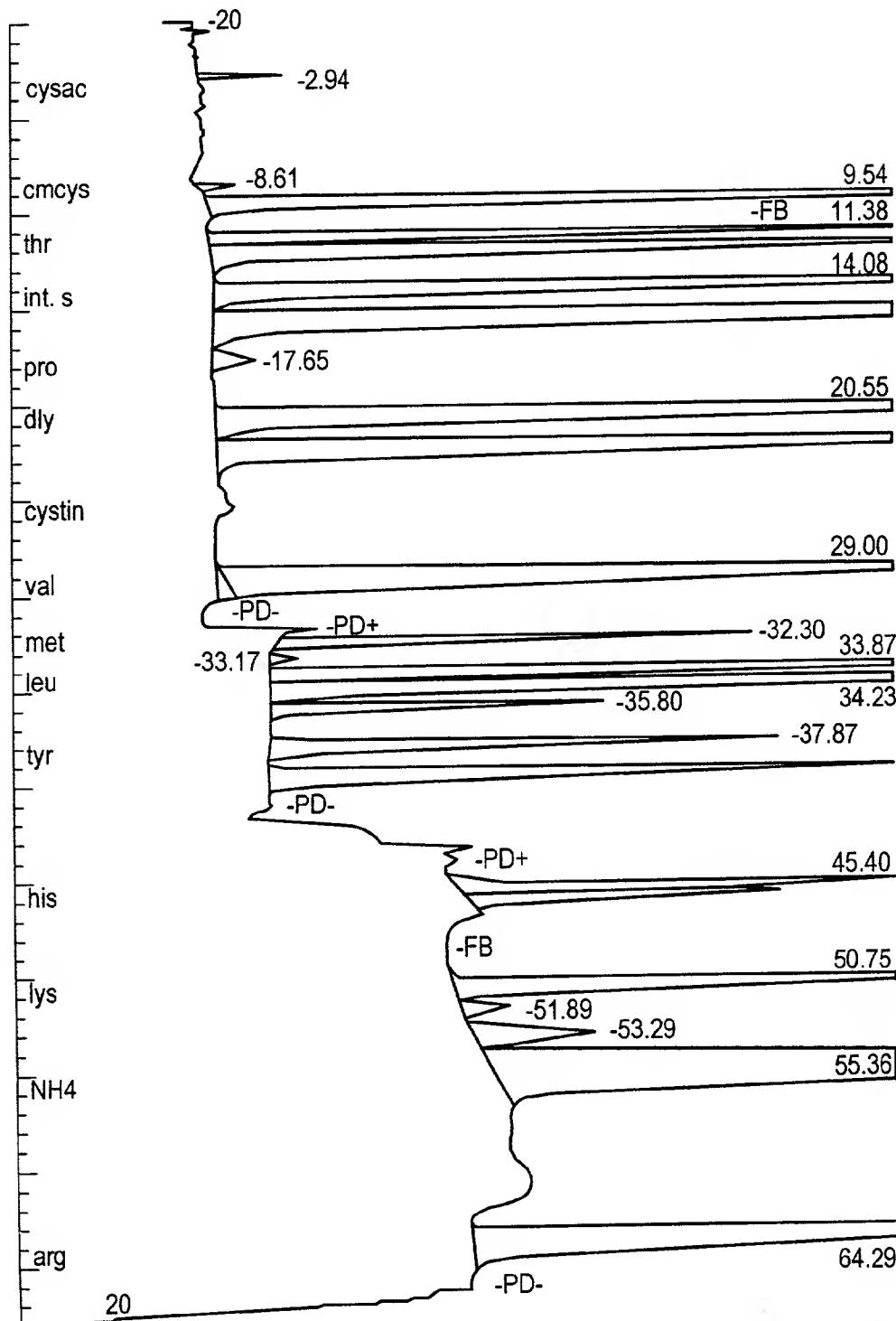
PEAK NUM	RET TIME	PEAK NAME	CONCENTRATION in nmoles	NORMALIZED CONC	AREA	HEIGHT	AREA/ HEIGHT	BL	REF PEAK	% DELTA RET TIME	CONC/ AREA
1	2.936			0.1504%	20695	1550	13.4	1	6	-1.592	3.4373E-06
2	8.609			0.0856%	9566	096	13.7	1	6	0	4.28185-06
3	9.543	asx		3.6346	7.6853%	1019304	61489	16.6	1	.5811	3.5658E-06
4	11.378	thr		1.1549	2.4420%	314916	15245	20.7	2	.1132	3.6674E-06
5	12.112	ser		2.0456	4.3254%	595007	27668	21.5	2	0	3.4380E-06
6	14.081	int. std.		1.0397	2.1985%	576309	23599	24.4	2	0	1.0041E-06
7	15.649	glx		6.6195	13.9567%	1959672	71617	27.4	2	.1667	3.3779E-06
8	17.651	pro+cys		2.1133	6.1414%	28161	809	34.8	2	.2854	1.0314E-04
9	20.554	gly		3.4509	7.2968%	1098728	36599	30.0	2	0	3.1408E-06
10	22.256	ala		2.8168	5.9961%	801412	25276	31.7	2	0	3.5248E-06
11	28.996	val		2.6160	5.4358%	783543	16490	42.7	1	0	3.6541E-06
12	32.299	set		0.5625	1.1894%	157161	8772	17.9	1	.0101	3.5792E-06
13	33.166			0.0000	0.0000%	10132	523	19.4	1	0.0000E+00	
14	33.967	ileu		1.8404	3.8914%	535119	23330	22.9	2	.0931	3.4392E-06
15	34.735	leu		3.1701	6.7031%	953284	38035	25.1	2	0	3.3255E-06
16	35.902	nl-std.		6.2739	0.5791%	163238	6196	26.3	2	0	1.6777E-06
17	37.871	tyr		1.0645	2.2508%	290327	9412	30.8	1	0	3.6666E-06
18	39.473	phe		1.6115	3.4075%	408260	12881	31.7	1	0	3.9472E-06
19	45.479	his		1.2110	2.6711%	203562	8185	24.9	2	0	0.0000E+00
20	46.013			0.0000	0.0000%	154147	5442	26.3	2	0	3.2302E-06
21	50.751	lys		1.2451	2.6327%	385456	13267	29.1	2	0	5.7275E-06
22	51.885				0.3929%	32441	913	35.5	2	0	0.0000E+00
23	53.287			0.0000	0.0000%	102408	2246	46.6	2	0	1.7279E-06
24	55.355	NH4		6.1666	13.0391%	3568874	61870	57.7	2	0	3.5009E-06
25	64.197	arg		3.5602	7.5279%	1016938	22156	45.9	1	0	
		TOTAL AMOUNT:			47.2934						

FIG. 5a2

47.2934

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AREAS, TIMES, AND HEIGHTS STORED IN : K: AAA936.ATB
DATA FILE = K: AAA936.PTS PRINTED ON 11-22-2000 AT 14:27:06
START TIME : 0.00 min. STOP TIME : 68.00 min. OFFSET : 0 mv
FULL RANGE : 15 millivolts



F I G. 5b

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EXTERNAL STANDARD TABLE

***** Sample Name: amino acid analysis 11-22-2000 14 : 28 : 43 Version 4.1 *****

Data File: K:BAA936

Date: 11-22-2000 14 : 26 : 30 Method: F:REBECKA

Interface: 0 Cycle #: 936 Operator jmc

Starting Peak Width: 21 Threshold: .5 Area Threshold: 500

Starting Delay: 0.00

Area reject: 5000

Amount injected: 1.00

Sample weight: 1.000000

PEAK NUM	RET TIME	PEAK NAME	CONCENTRATION in nmoles	NORMALIZED CONC	AREA	HEIGHT	AREA/ BL	REF PEAK	% DELTA	CONC/ AREA
1	8.775		0.0000	0.00000%	5143	286	18.0	1		0.0000E+00
2	9.510		0.0000	0.00000%	129394	7707	16.8	1		0.0000E+00
3	11.345		0.0000	0.00000%	24969	1171	21.3	2		0.0000E+00
4	12.079		0.0000	0.00000%	59106	2389	24.7	2		0.0000E+00
5	14.047		0.0000	0.00000%	47121	1978	23.8	1	.2393	0.0000E+00
6	15.616	glx	6.2317	74.6757%	375516	13802	27.2	1	7	0
7	17.651	pro+cys	(2.1133)	25.3244%	199944	6665	30.0	1	7	1.6595E-05
8	20.554		0.0000	0.00000%	83682	2753	30.4	1		1.0570E-05
9	22.222		0.0000	0.00000%	67237	2027	33.2	1		0.0000E+00
TOTAL AMOUNT:			8.3451							

SEE FIG. 5c2

FIG. 5c1

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SEE FIG. 5c1

AREAS, TIMES, AND HEIGHTS STORED IN: K: BAA936.ATB
DATA FILE = K: BAA936.PTS PRINTED ON 11-22-2000 AT 14:28:59
START TIME : 0.00 min. STOP TIME : 68.00 min. OFFSET : -95 mv
FULL RANGE : 15 millivolts

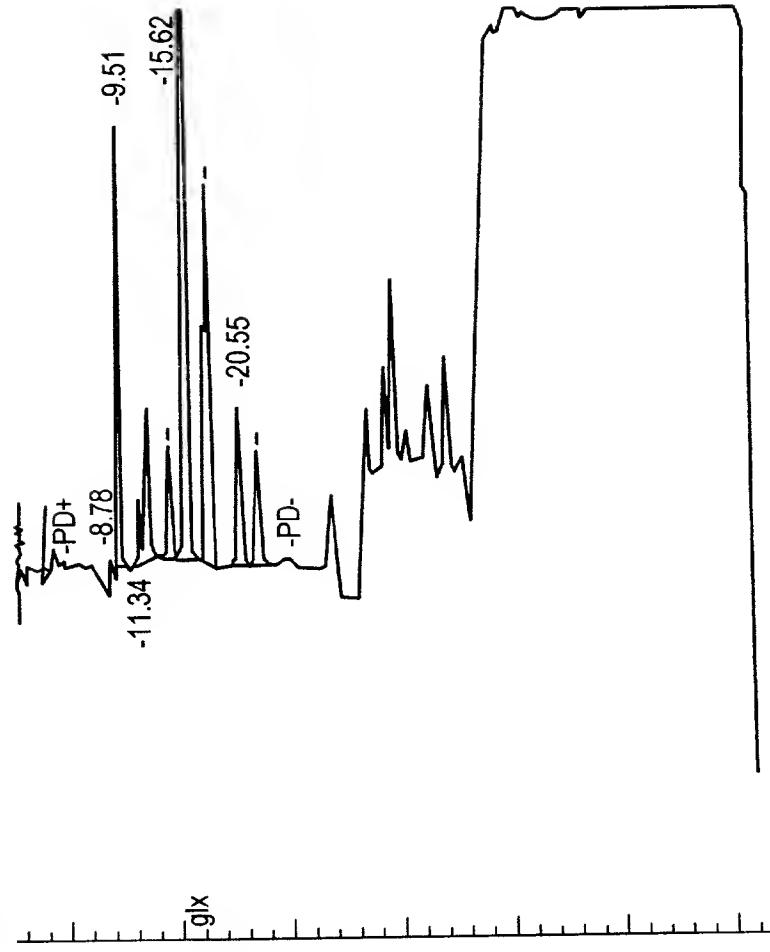


FIG. 5c2